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Evaluating Forensic DNA Evidence

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Evaluating forensic DNA evidence

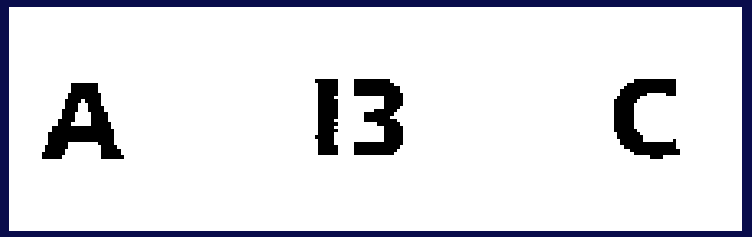
Dan E. Krane, Wright State University, Dayton, OH

Steelman Visiting Scientist Lecture Series, Lenoir-Rhyne University, April 9, 2010

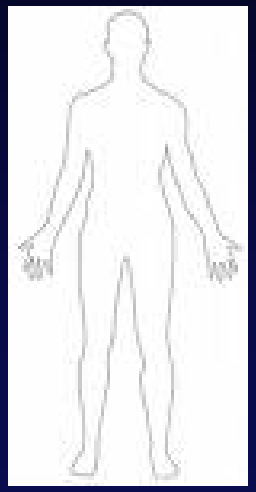
Forensic Bioinformatics
(www.bioforensics.com)

The science of DNA profiling is sound.

But, not all of DNA profiling is science.

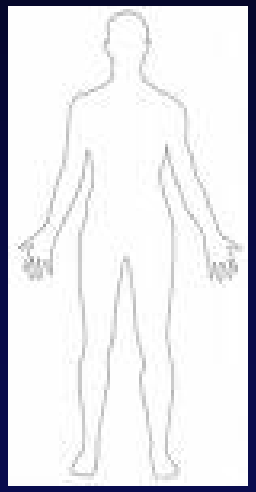

A 13 C

DNA content of biological samples



Trillions of cells

DNA content of biological samples

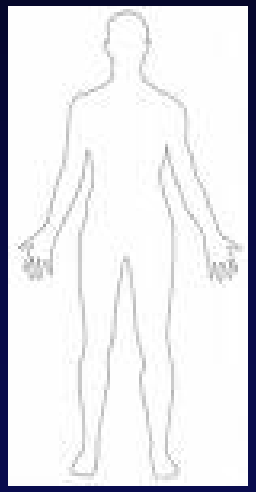


Trillions of cells

QuickTime™ and a
TIFF (Uncompressed) decompressor
are needed to see this picture.

Roughly 100 cells

DNA content of biological samples



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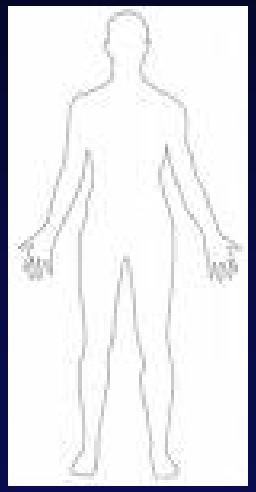
Roughly 100 cells

Each cell contains 6 to 7 pg of DNA

DNA profiling kits generally recommend using between 500 and 1,000 pg of template DNA

DNA content of biological samples



Trillions of cells

QuickTime™ and a
TIFF (Uncompressed) decompressor
are needed to see this picture.

Roughly 100 cells

Each cell contains 6 to 7 pg of DNA

DNA profiling kits generally recommend using between 500 and 1,000 pg of template DNA

That works out to roughly 100 to 200 cells

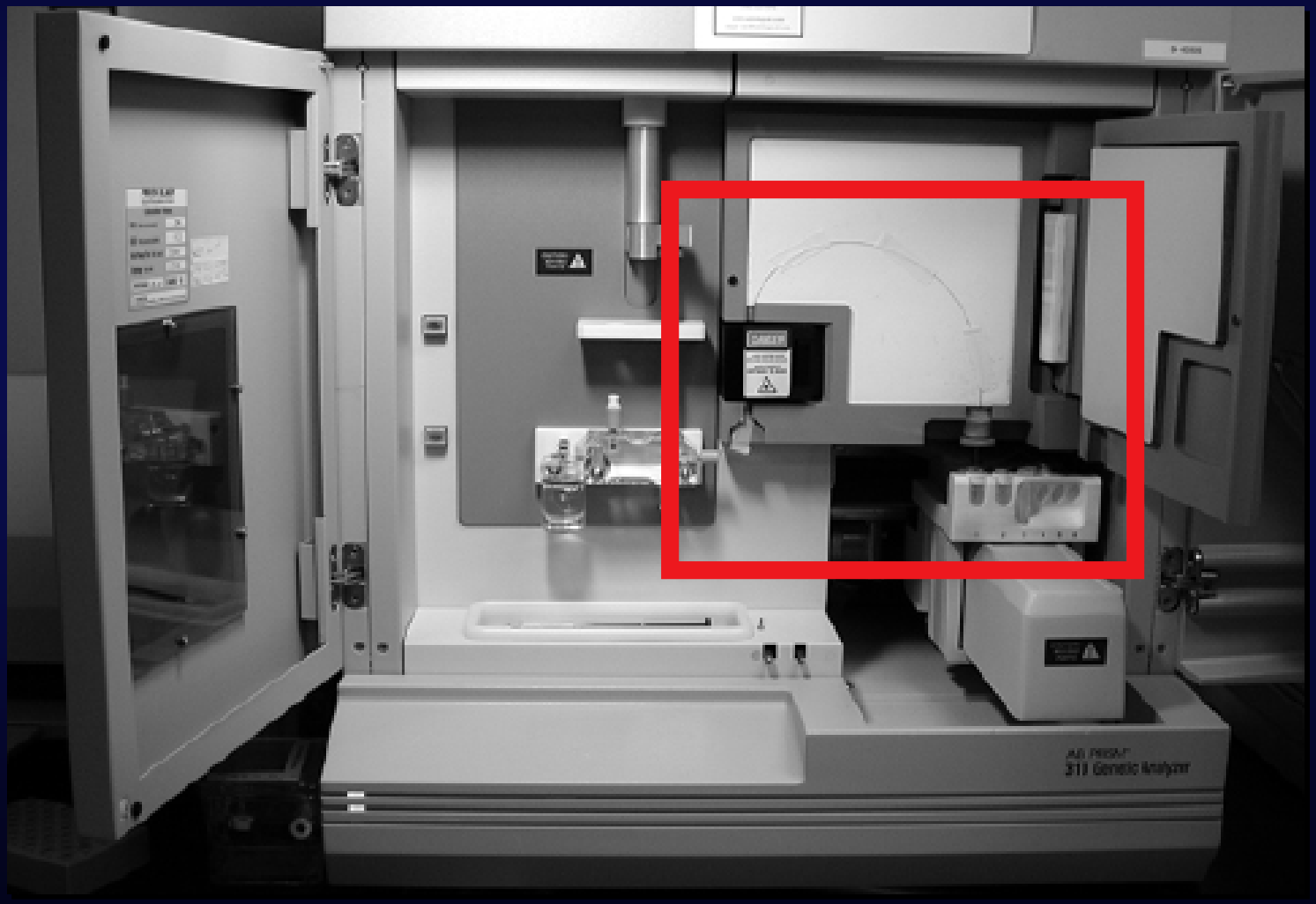
Crime Scene Samples & Reference Samples

- Extract and purify DNA

PCR Amplification

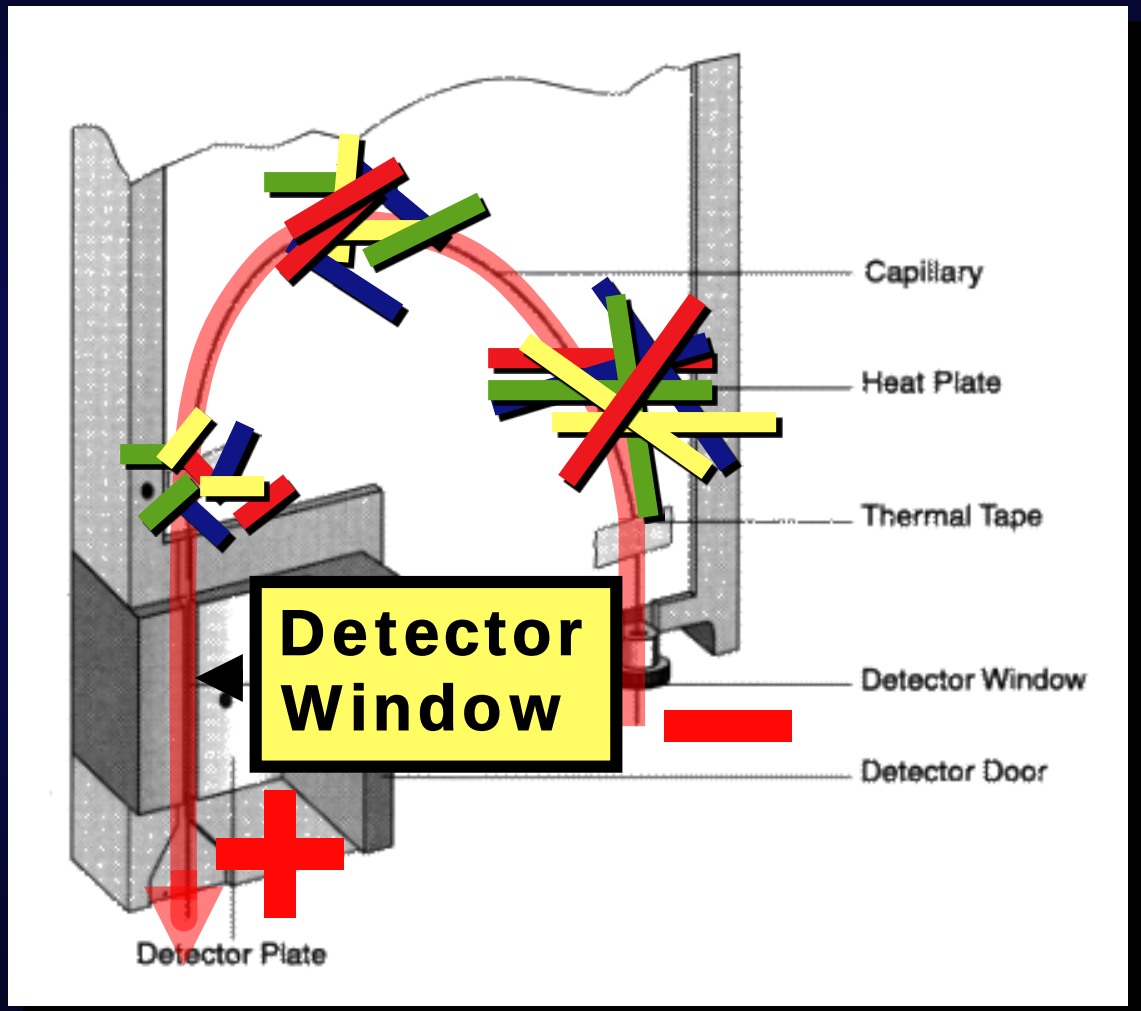
- DNA regions flanked by primers are amplified

The ABI 310 Genetic Analyzer

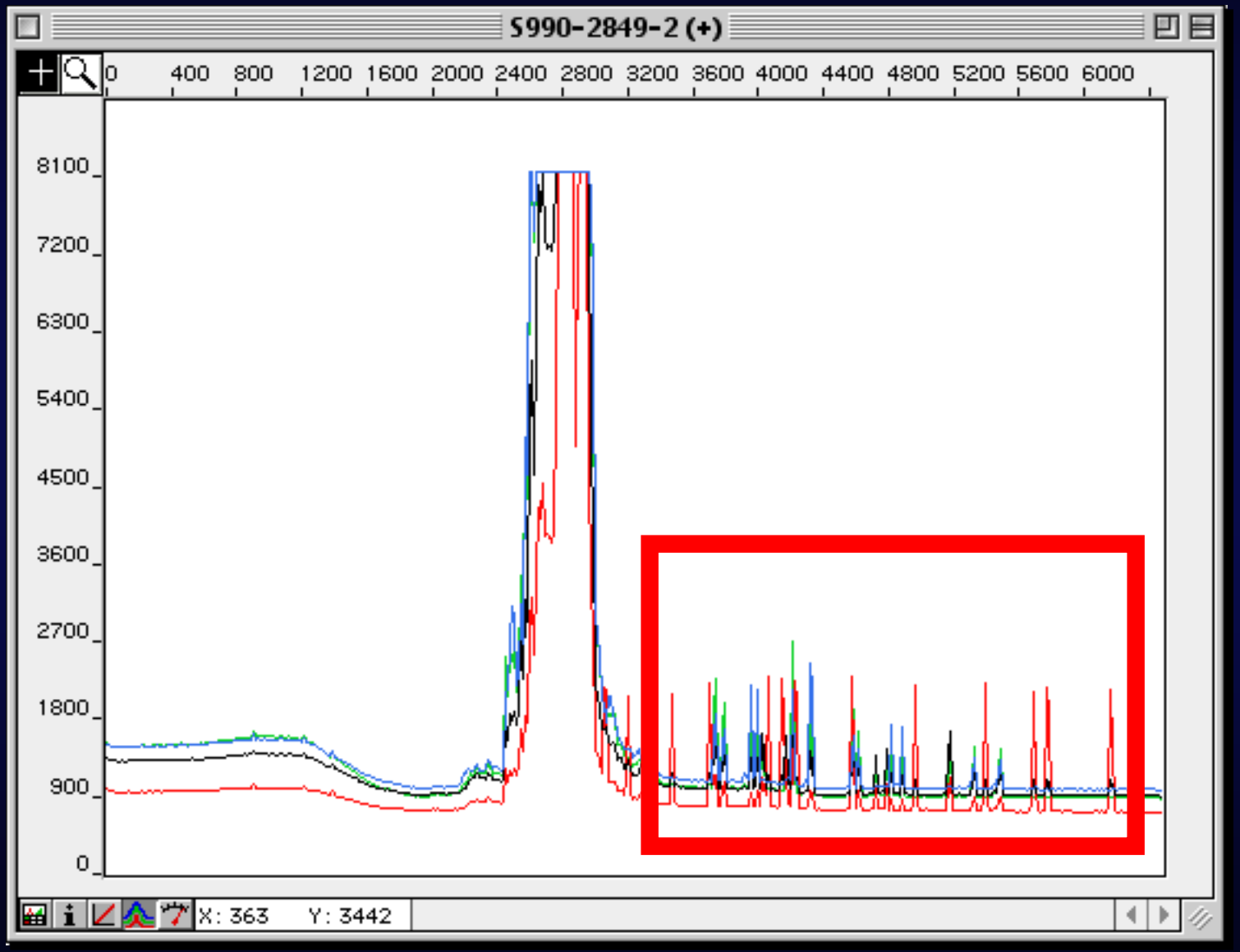


ABI 310 Genetic Analyzer: Capillary Electrophoresis

- Amplified STR DNA injected onto column
- Electric current applied
- DNA pulled towards the positive electrode
- DNA separated out by size:
  - Large STRs travel slower
  - Small STRs travel faster
- Color of STR detected and recorded as it passes the detector



Profiler Plus: Raw data



Statistical estimates: the product rule

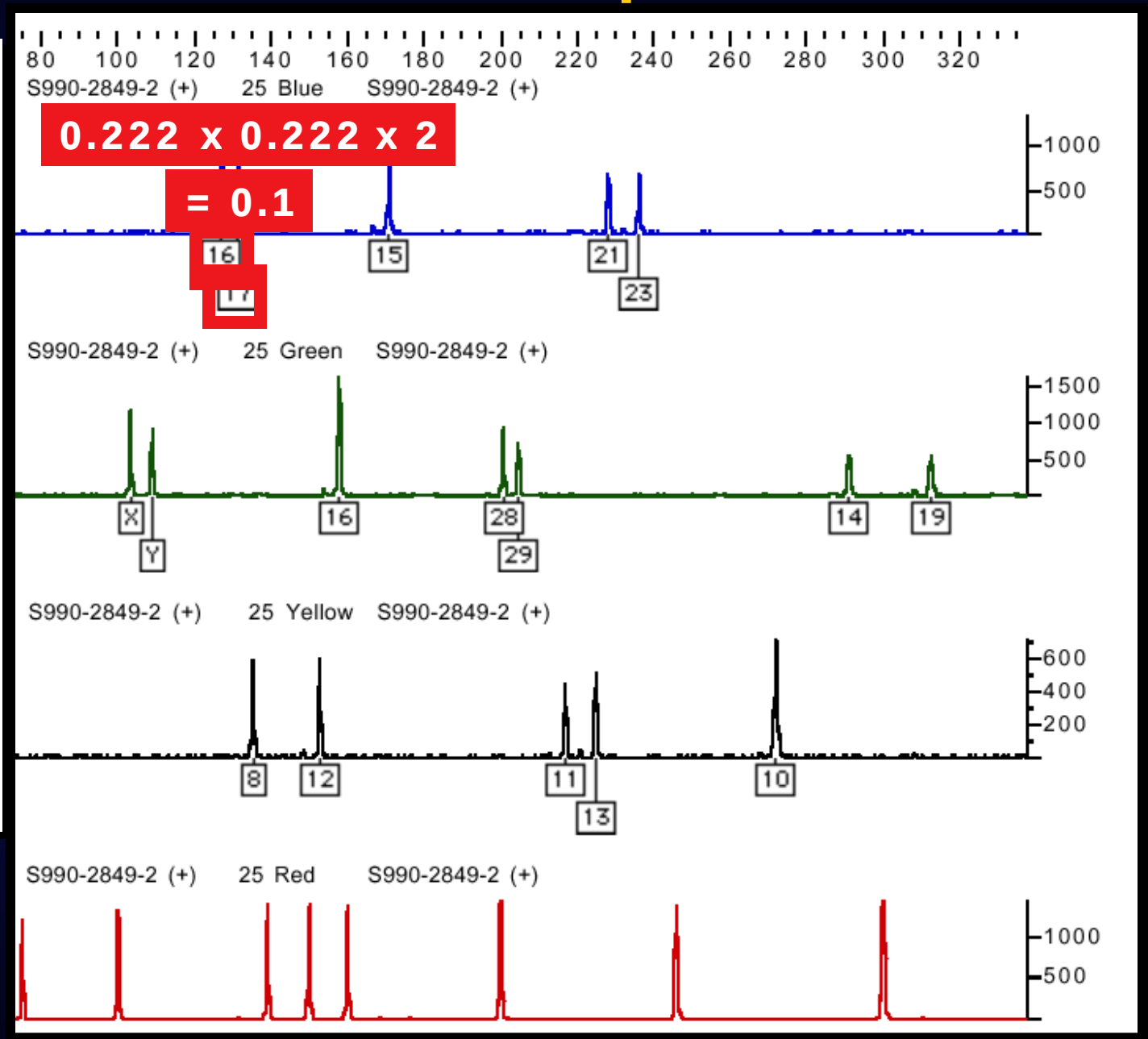
Allele Frequencies

Locus D3S1358
Race Caucasian
(N = 203)

Allele	Frequency
12	0.012
13	0.012
14	0.140
[redacted]	[redacted]
19	0.012

Locus vWA
Race Caucasian
(N = 196)

Allele	Frequency
11	0.012
12	0.012
13	0.012
14	0.102
15	0.082



Statistical estimates: the product rule

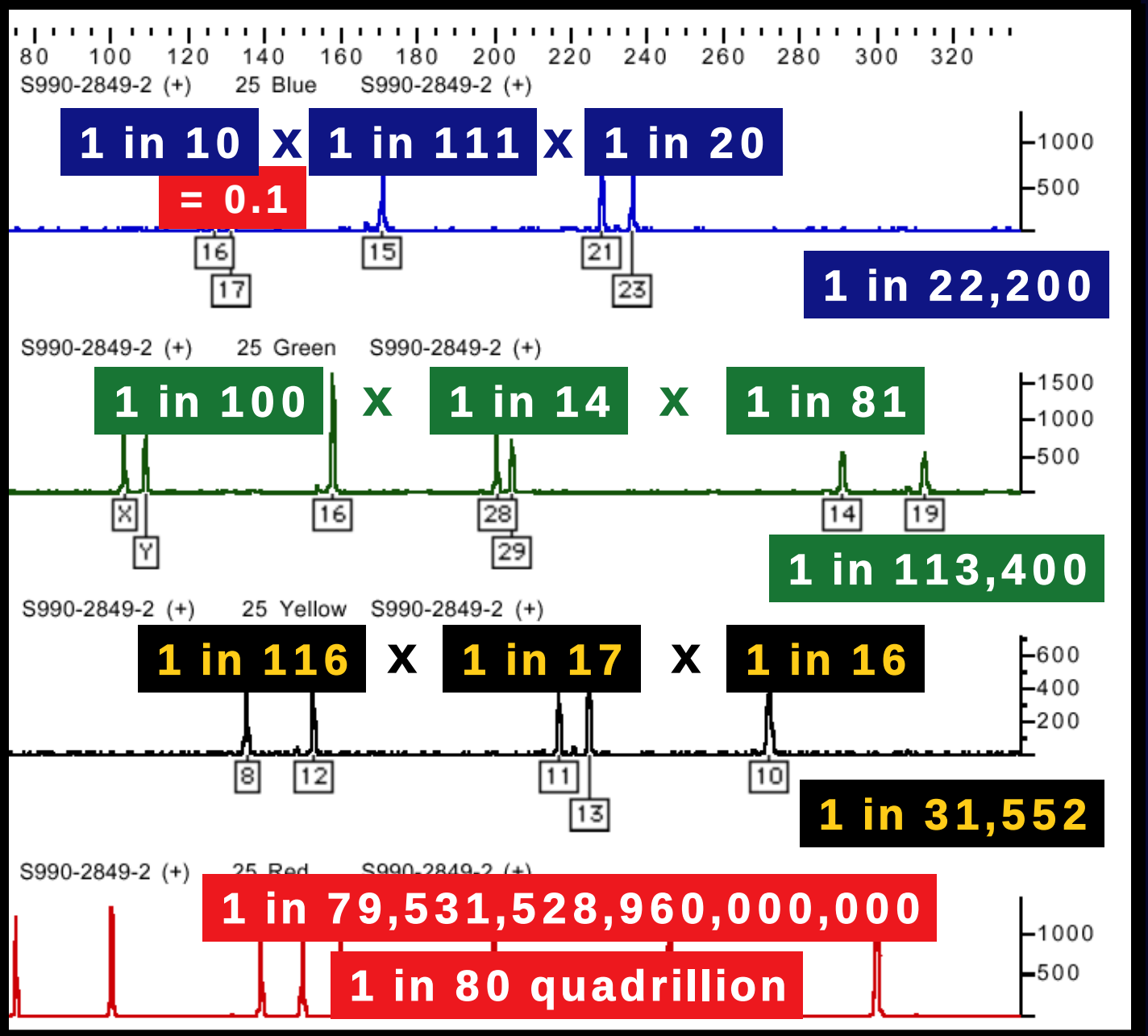
Allele Frequencies

Locus D3S1358
Race Caucasian
(N = 203)

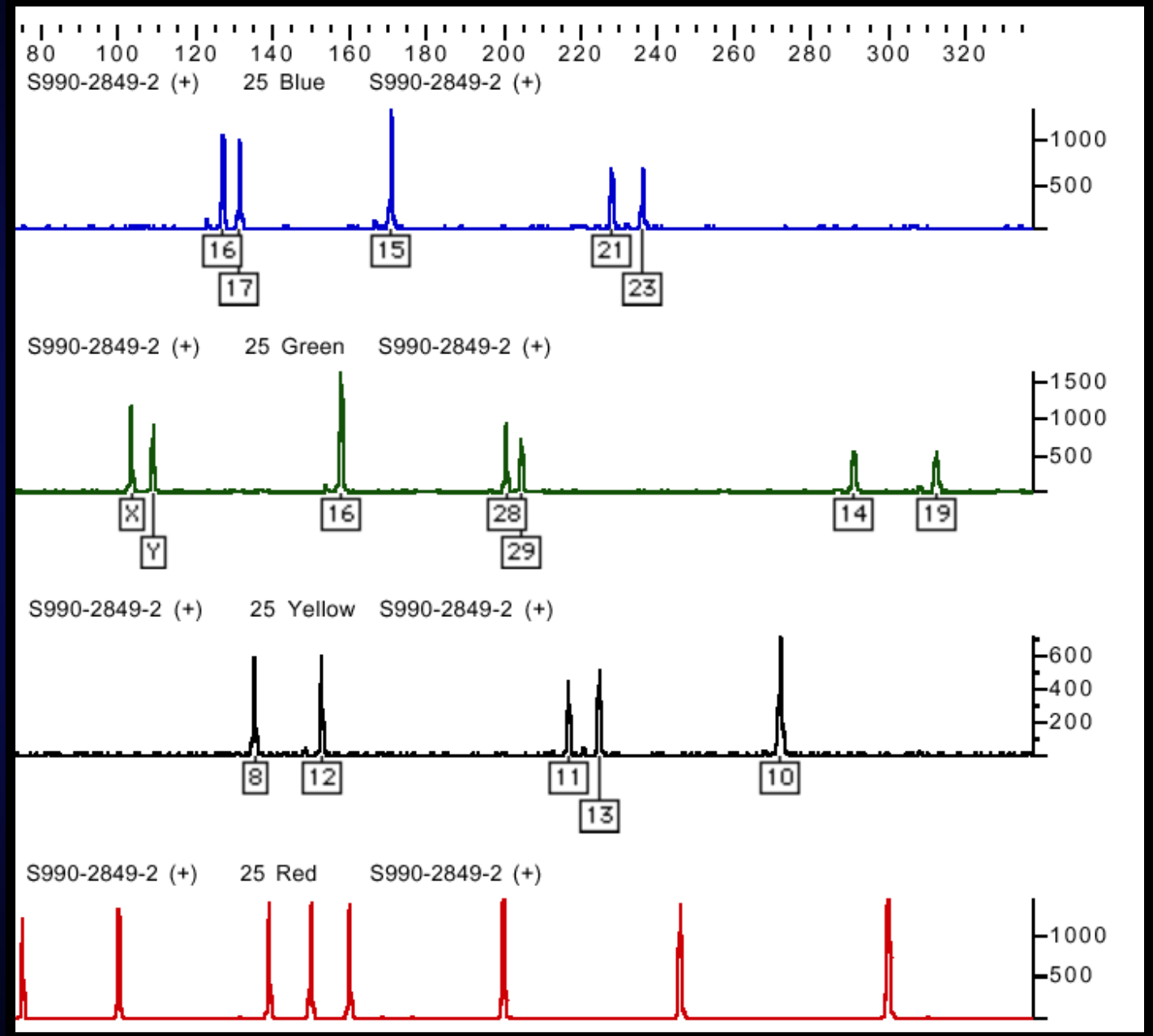
Allele	Frequency
12	0.012
13	0.012
14	0.140
15	0.246
16	0.222
17	0.222
18	0.163
19	0.012

Locus vWA
Race Caucasian
(N = 196)

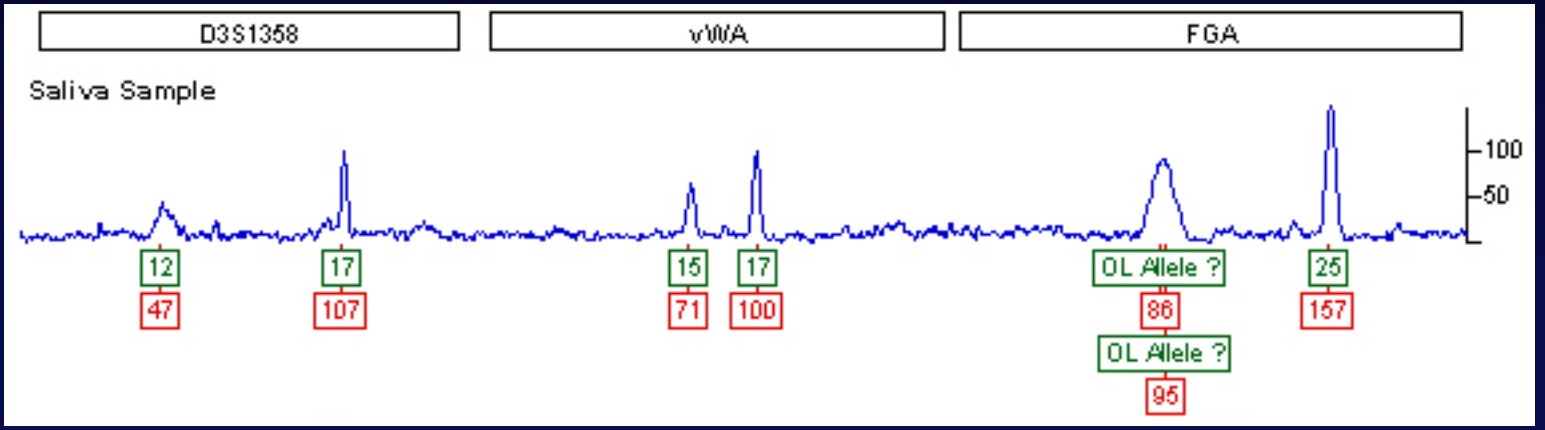
Allele	Frequency
11	0.012
12	0.012
13	0.012
14	0.102
15	0.082



Doesn’t someone either match or not?



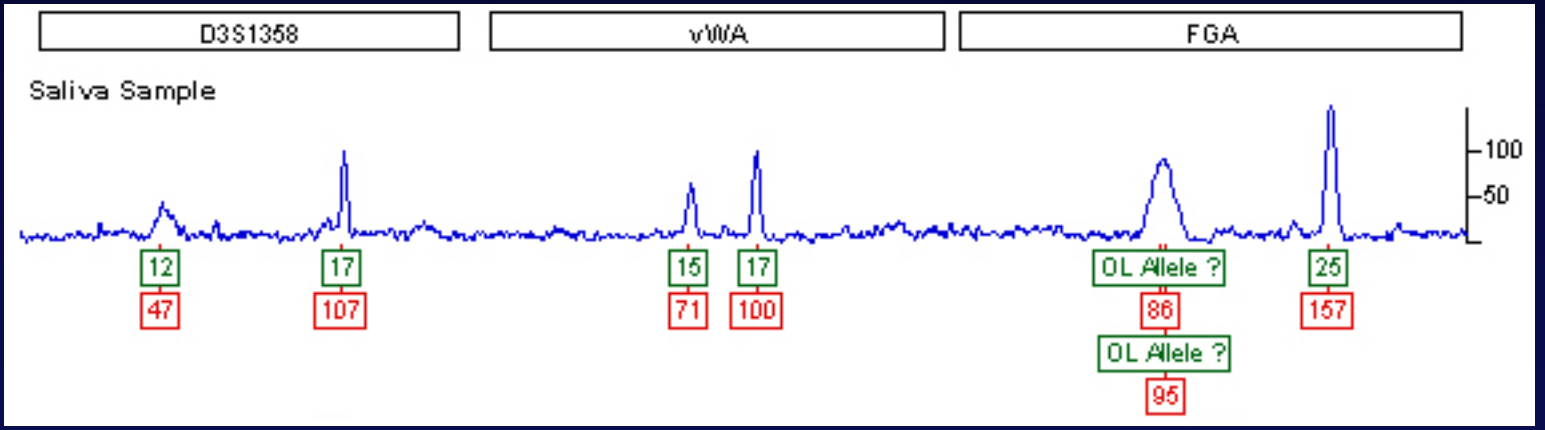
Opportunities for subjective interpretation?



Can “Tom” be excluded?

Suspect	D3	vWA	FGA
Tom	17, 17	15, 17	25, 25

Opportunities for subjective interpretation?

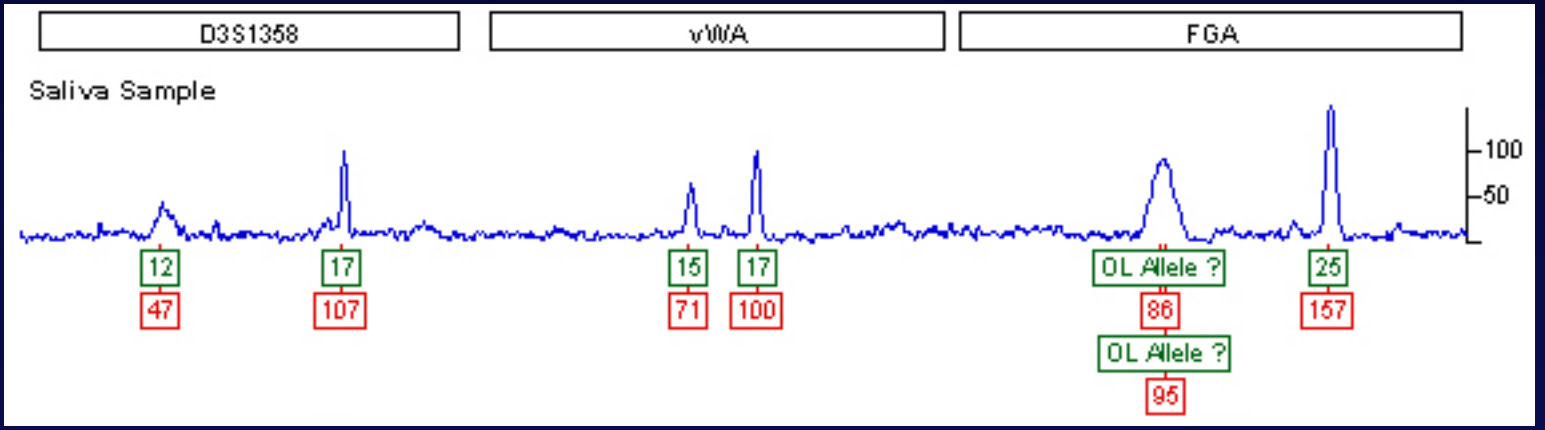


Can “Tom” be excluded?

Suspect	D3	vWA	FGA
Tom	17, 17	15, 17	25, 25

No -- the additional alleles at D3 and FGA are “technical artifacts.”

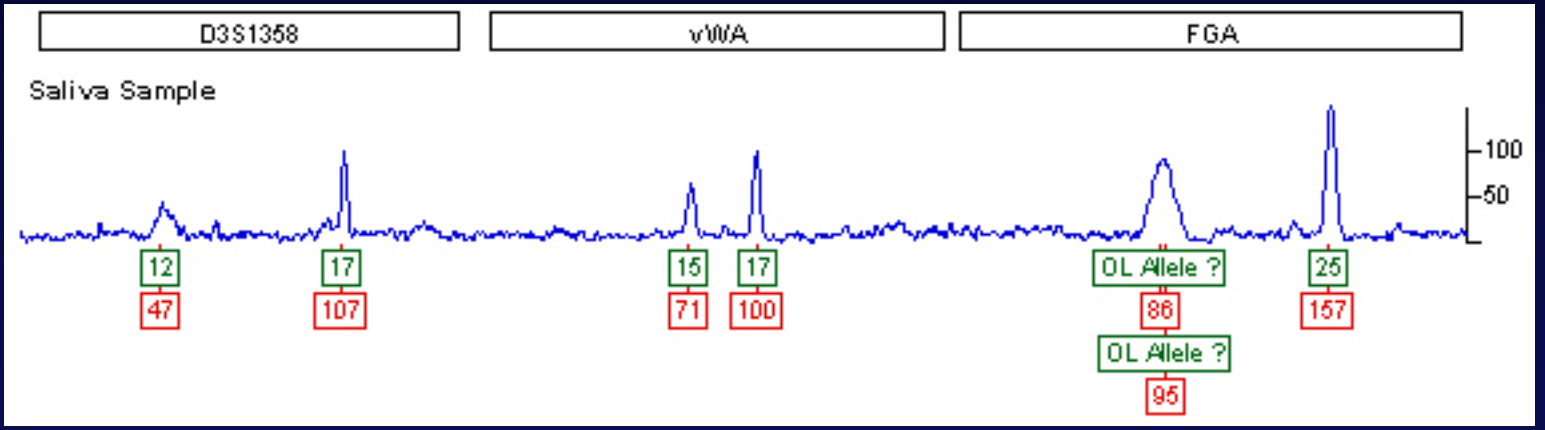
Opportunities for subjective interpretation?



Can “Dick” be excluded?

Suspect	D3	vWA	FGA
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25

Opportunities for subjective interpretation?

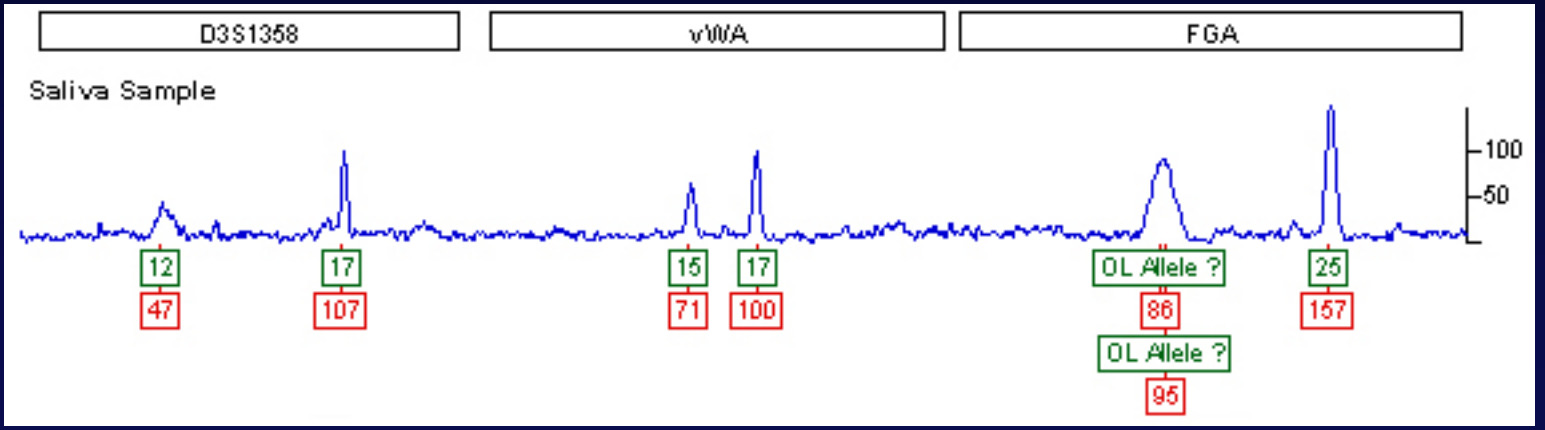


Can “Dick” be excluded?

Suspect	D3	vWA	FGA
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25

No -- stochastic effects explain peak height disparity in D3; blob in FGA masks 20 allele.

Opportunities for subjective interpretation?

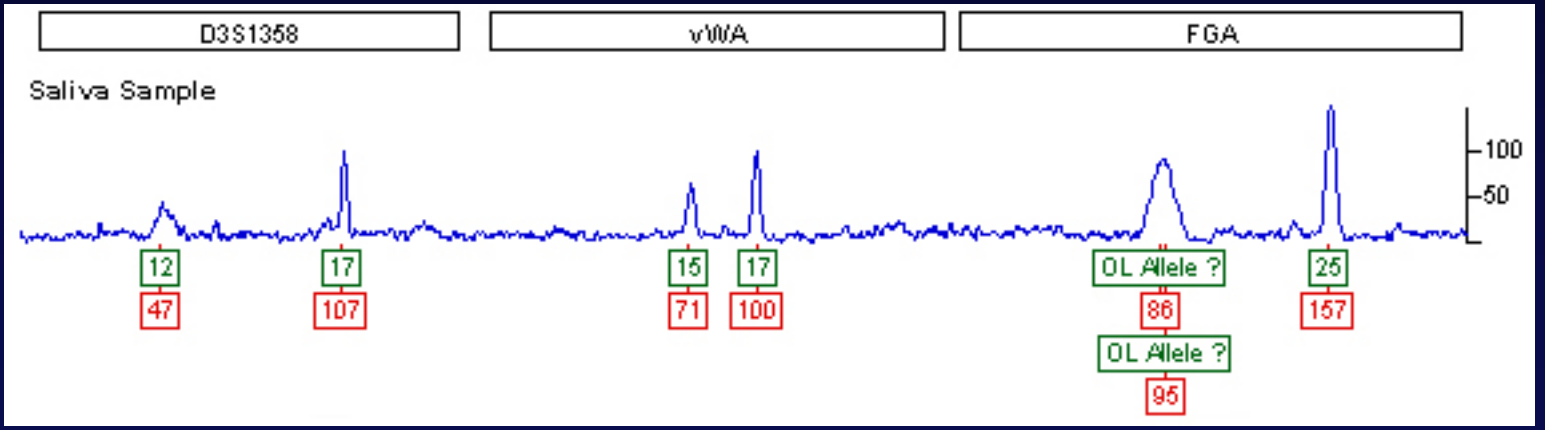


Can “Harry” be excluded?

Suspect	D3	vWA	FGA
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25
Harry	14, 17	15, 17	20, 25

No -- the 14 allele at D3 may be missing due to “allelic drop out”; FGA blob masks the 20 allele.

Opportunities for subjective interpretation?



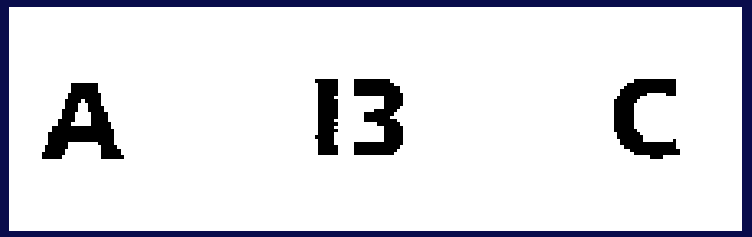
Can “Sally” be excluded?

Suspect	D3	vWA	FGA
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25
Harry	14, 17	15, 17	20, 25
Sally	12, 17	15, 15	20, 22

No -- there must be a second contributor; degradation explains the “missing” FGA allele.

Observer effects, aka context effect

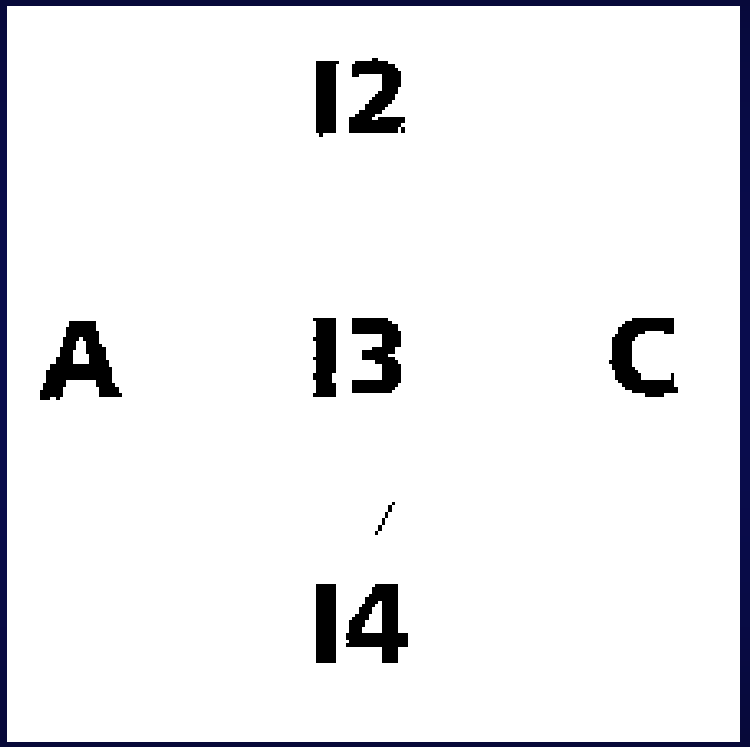
- *--the tendency to interpret data in a manner consistent with expectations or prior theories (sometimes called “examiner bias”)*


A 13 C

12

13

14


12
A
13
C
14

Observer effects, aka context effect

- *--the tendency to interpret data in a manner consistent with expectations or prior theories (sometimes called “examiner bias”)*
- Most influential when:
  - Data being evaluated are ambiguous or subject to alternate interpretations
  - Analyst is motivated to find a particular result

Analyst often have strong expectations about the data

DNA Lab Notes (*Commonwealth v. Davis*)

- *"I asked how they got their suspect. He is a convicted rapist and the MO matches the former rape…The suspect was recently released from prison and works in the same building as the victim…She was afraid of him. Also his demeanor was suspicious when they brought him in for questioning…He also fits the general description of the man witnesses saw leaving the area on the night they think she died…So, I said, you basically have nothing to connect him directly with the murder (unless we find his DNA). He said yes."*

Analyst often have strong expectations about the data

DNA Lab Notes

- *"Suspect-known crip gang member--keeps 'skating' on charges-never serves time. This robbery he gets hit in head with bar stool--left blood trail. Miller [deputy DA] wants to connect this guy to scene w/DNA ..."*

Analyst often have strong expectations about the data

DNA Lab Notes

- *"Suspect-known crip gang member--keeps 'skating' on charges-never serves time. This robbery he gets hit in head with bar stool--left blood trail. Miller [deputy DA] wants to connect this guy to scene w/DNA …"*

"Death penalty case! Need to eliminate Item #57 [name of individual] as a possible suspect"

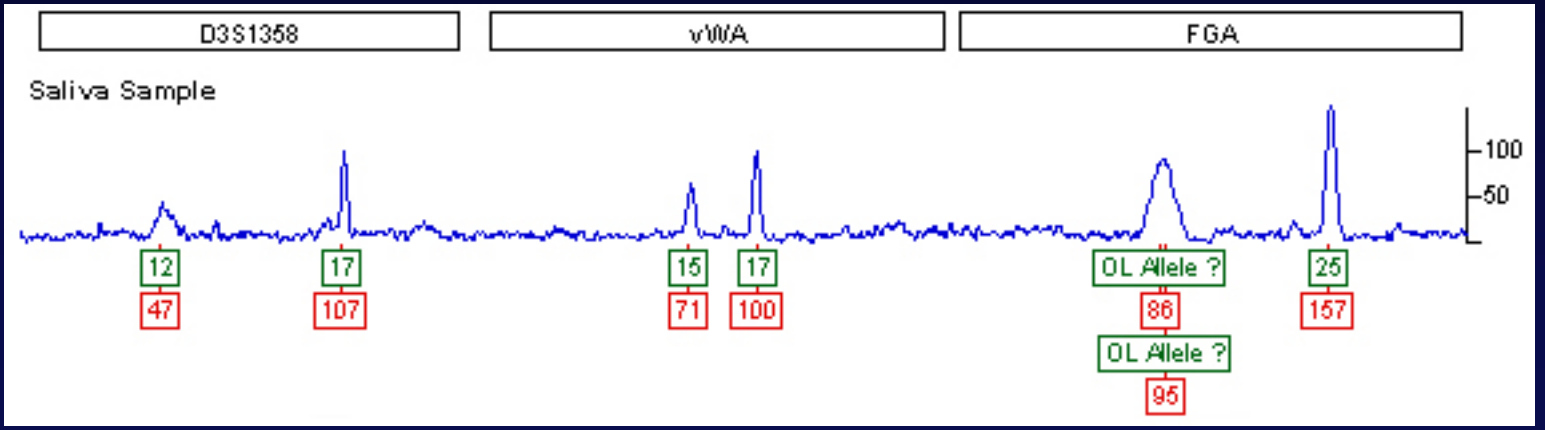
Analysts' expectations may lead them to:

- Resolve ambiguous data in a manner consistent with expectations
- Miss or disregard evidence of problems
- Miss or disregard alternative interpretations of the data
- Thereby undermining the scientific validity of conclusions
  - *See*, Risinger, Saks, Thompson, & Rosenthal, *The Daubert/Kumho Implications of Observer Effects in Forensic Science: Hidden Problems of Expectation and Suggestion*. 93 California Law Review 1 (2002).

Sequential unmasking: a remedy for context effects

- Simply interpret evidence with no knowledge of reference samples
- Minimizes subjectivity of interpretations
- Forces analysts to be truly conservative in their interpretations

Opportunities for subjective interpretation?



Who can be excluded?

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Harry	14, 17	15, 17	20, 25
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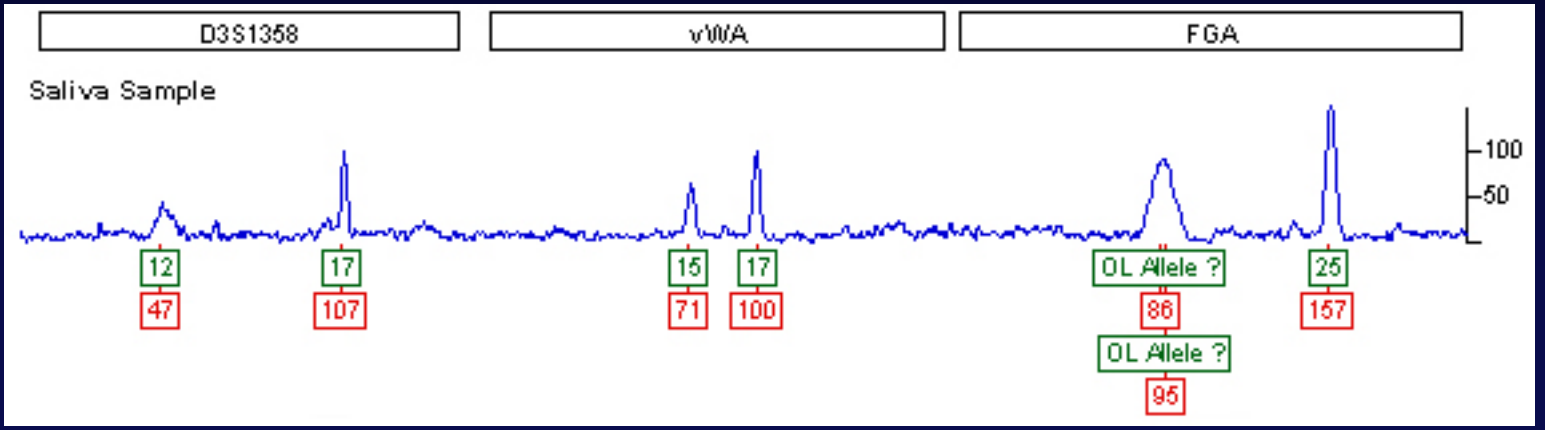

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Sequential unmasking: a remedy for context effects

- Simply interpret evidence with no knowledge of reference samples
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Sequential unmasking: a remedy for context effects

- Simply interpret evidence with no knowledge of reference samples
- Minimizes subjectivity of interpretations
- Forces analysts to be truly conservative in their interpretations
- Is it possible to do this for *all* forensic science?

Documenting errors:
DNA Advisory Board Quality Assurance Standards for Forensic DNA Testing Laboratories, Standard 14

[Forensic DNA laboratories must] “follow procedures for corrective action whenever proficiency testing discrepancies and/or casework errors are detected” [and] “shall maintain documentation for the corrective action.”

Documenting errors

Positive result in negative control, due to tube swap:

Conclusion:

When the data was analyzed as a whole before separating into mini projects, it was clear to see that the tubes in positions D2 and D4 were switched on accident. On the Injection list, the D2 position was labeled as the negative control (A5731) however the data shows a profile consistent with PI-09 in COfiler. The D4 position that was labeled PI-09 (A2637R) shows a profile consistent with that of a negative control.

Corrective Action for future analyses BS.-

Consecutively label 310 tubes, as well as, number w/ DNA numbers.

Check tubes carefully when placing in 310 tube racks.

02274

Documenting errors

Analyst contamination:

Contamination of Known Reference Sample:

On March 7, 2003 it was discovered that the known reference sample for victim Gilbert Osorno, Lab #PE02-00459-02, was contaminated with the Analyst, Vickie Kump's, DNA profile. It could not be determined how or at what stage of the analysis the contamination occurred. The analyst repeated the analysis using the same lab protocols as used previously resulting in a single profile of the victim.

Documenting errors

Separate samples combined in one tube . . . .

Sample Handling Problem During Extraction of Evidence Items for PE96-00286 and PE02-00405

On April 29, 2002 during the extraction procedure for evidence items in Lab Number PE96-00286-03 the extract for A3822 was inadvertently added to the Centricon that already contained the extract for sample A3821. The problem was

Documenting errors

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. . . . leading to corrective action:

Corrective Action

Try to minimize interruptions during any sample transfer procedures. Signs were made for the analysts to put at the end of their work areas indicating that they cannot be interrupted at the time the sign is out. Also, phone calls will not be answered during any sample handling and transfer steps.

Documenting errors

Suspect doesn't match himself . . . .

On 5/16/01, we had reported another case (PA01-00171) involving Mr. Phillips. The genetic profiles generated for Mr. Phillips in these two cases differed at all loci tested. Clearly, at least one had to be erroneous. I left a note for Vickie Kump (who was preparing to generate the draft

. . . . but then, staff is "'always' getting people's names wrong":

Case Processing Form" (see attached #4) released [illegible]

from Terry Phillips. I immediately asked Paul why he had not noted of followed up on the difference between the name "Lucio Flores" on both the sample envelope and swab, and "Terry Phillips" on the appointment slip and COC forms. He responded that he did not expect to have to do someone else's job for them, and that they [collection room staff] are 'always' getting people's names wrong, so he only goes by the case number not the name. In addition, he later told me that during pre-extraction sample processing, he fills out the sample identifiers on the case processing form prior to (not during) sample examination.

The science of DNA profiling is sound.

But, not all of DNA profiling is science.

This is especially true in situations involving: small amounts of starting material, mixtures, relatives, and analyst judgment calls.